

Sat Oct 12 13:34:36 2002

Claim 6; Page 30; 37pp; English.

PS This invention describes novel G protein-coupled receptor agonists or  
CC antagonists which specifically bind to the juxtamembrane extracellular  
CC structural elements of the G protein-coupled receptor in a manner  
CC different from that of the natural ligand and where the agonist or  
CC antagonist alters the transduction of an intracellular signal. The  
CC products of the invention have gynecological and analgesic activity. The  
CC G protein-coupled receptor antagonist or its functional derivatives is  
CC useful for preventing premature delivery of fetus, and for preventing  
CC and/or treating dysmenorrhea. AA87609-Y87620 represent G  
CC protein-coupled receptor/antagonist peptide fragments which are described  
CC in the method of the invention.

XX Sequence 8 AA;

SQ Query Match 100.0%; Score 45; DB 21; Length 8;

Best Local Similarity 100.0%; Pred. No. 6.4e+05; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8  
| | | | | | | |

DB 1 ILGHRDYK 8  
| | | | | | | |

RESULT 2

AA869546  
ID AAR69546 standard; Protein; 359 AA.

XX AC

XX AC

XX 05-SEP-1995 (first entry)

XX Prostaglandin FP receptor protein.

XX Prostaglandin F2-alpha; PGF2-alpha; FP receptor;

KW activity modulators; glaucoma; oestrus cycle.

XX OS Homo sapiens.

XX WO9500551-A.

XX 05-JAN-1995.

XX 09-JUN-1994; 94WO-CA00319.

XX 25-JUN-1993; 93US-0083741.

XX (MERI ) MERCK FROSST CANADA INC.

XX Abramovitz M, Grygorczyk R, Metters K, Nguyen T;

PI Rushmore TH, Slipetz D;

XX WPI; 1995-052011/07.

DR N-PSDB; AAQ81959.

XX New prostaglandin FP receptor and DNA - used partic. to identify  
XX modulators of prostaglandin receptor activity for treatment of  
XX diseases.

PS Claim 2; Page 33; 46pp; English.

XX AAQ81959 encodes AAR69546 the prostaglandin (PG) FP receptor, to  
CC which PGF2-alpha binds. The protein can be used to identify  
CC modulators of PG receptor activity (claimed), useful in the  
CC treatment of PG-related diseases. Selective agonists of the  
CC FP receptor may be used to treat glaucoma or to synchronise  
CC oestrus cycles in farm animals

XX Sequence 359 AA;

Query Match 100.0%; Score 45; DB 16; Length 359;

Best Local Similarity 100.0%; Pred. No. 0.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8  
| | | | | | | |

DB 171 ILGHRDYK 178  
| | | | | | | |

RESULT 3

AA873410  
ID AAR73410 standard; Protein; 359 AA.

XX AC

XX AC

XX 25-SEP-2000 (first entry)

XX Human FP prostaglandin.

XX Prostaglandin; receptor; pulmonary system; glaucoma;

KW identification; allele; polymorphism; detection; prostanoid; FP;

KW IP; DP; EP; TP; human.

XX OS Homo sapiens.

XX WO200029614-A1.

XX 25-MAY-2000.

XX 12-NOV-1998; 98WO-IB01803.

XX 12-NOV-1998; 98WO-VB01803.

XX (EURO-) EURONA MEDICAL AB.

XX Jonsson L, Lindstroem HR;

XX WPI; 2000-387820/33.

XX N-PSDB; AA293893.

XX Assessing prostanoid response status in an individual suffering from  
XX prostaglandin associated diseases such as pulmonary hypertension,  
XX glaucoma or arteriosclerosis, comprises comparing polymorphic patterns  
XX Claim 18; Fig 1; 57pp; English.

XX The prostaglandin receptor family encompasses at least five classes  
XX of receptors designated FP, EP, IP, DP and TP receptors which are  
XX classified based on their sensitivity to the five primary prostanoids  
XX (F2alpha, E2, I-2, D-2 and TXA2). EP receptors further comprise  
XX four subtypes, designated EPI-4, which differ in their responses to  
XX various agonists and antagonists. The receptors have also shown a  
XX degree of cross reactivity. They may derive from a common ancestral  
XX gene. All of the receptors may exist as allelic variants and these  
XX polymorphisms may have an effect on a patient's reaction to  
XX prostanoids. Detection of these polymorphisms may identify patients  
XX at risk from toxic or abnormal responses to prostanoid treatment.  
XX The prostaglandins play a role in the pulmonary system and in  
XX glaucoma.

SQ Sequence 359 AA;

Query Match 100.0%; Score 45; DB 21; Length 359;

Best Local Similarity 100.0%; Pred. No. 0.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8  
| | | | | | | |

DB 171 ILGHRDYK 178  
| | | | | | | |

RESULT 4

AA879542

ID AAR79542 standard; Protein; 362 AA.

XX

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:40:49 ; Search time 31 Seconds  
(without alignments)  
28.664 Million cell updates/sec

Title: US-09-787-334-1

Perfect score: 45

Sequence: 1 ILGHRDYK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	8	21	Murine G protein-c
2	45	100.0	359	16	Prostaglandin FP r
3	45	100.0	359	21	Human FP prostagla
4	45	100.0	362	16	Bovine prostagland
5	42	93.3	8	21	Murine G protein-c
6	41	91.1	8	21	Murine G protein-c
7	41	91.1	366	16	Mouse prostaglandi
8	40	88.9	7	21	Murine G protein-c
9	40	88.9	8	21	Murine G protein-c
10	39	86.7	8	21	Murine G protein-c
11	37	82.2	319	21	Mouse trypsin fami

12	36	80.0	8	21	AA187613	Murine G protein-c
13	36	80.0	8	21	AA187619	Murine G protein-c
14	35	77.8	8	21	AA187618	Murine G protein-c
15	35	77.8	131	21	AA187619	Human secreted pro
16	35	77.8	134	21	AA187619	Human secreted pro
17	35	77.8	187	21	AA187619	Human novel foetal
18	34	75.6	69	22	AA187619	Enterococcus faeca
19	34	75.6	571	20	AA187619	Enterococcus faeca
20	34	75.6	579	22	AA187619	Drosophila melanog
21	34	75.6	593	20	AA187619	Enterococcus faeca
22	33	73.3	366	15	AA187619	Prostaglandin rece
23	33	73.3	456	22	AA187619	Drosophila melanog
24	33	73.3	514	22	AA187619	Novel human diagno
25	32	71.1	111	22	AA187619	Propionibacterium
26	32	71.1	240	21	AA187619	Murine FGF-3 prote
27	32	71.1	245	19	AA187619	Fibroblast growth
28	32	71.1	245	22	AA187619	Murine fibroblast
29	32	71.1	329	22	AA187619	Propionibacterium
30	32	71.1	439	16	AA187619	WD-40 domain-contg
31	32	71.1	587	19	AA187619	A human chronic re
32	32	71.1	587	19	AA187619	A human chronic re
33	32	71.1	634	19	AA187619	Human protein sequ
34	32	71.1	634	22	AA187619	Human protein sequ
35	32	71.1	652	22	AA187619	Drosophila melanog
36	32	71.1	652	22	AA187619	Novel human diagno
37	32	71.1	696	22	AA187619	Human protein sequ
38	32	71.1	925	22	AA187619	A. mediterranei ri
39	32	71.1	4572	19	AA187619	NDMIS peptide desi
40	31	68.9	16	17	AA187619	Enterokinase site
41	31	68.9	21	15	AA187619	Human reproductiv
42	31	68.9	29	22	AA187619	Human breast or ov
43	31	68.9	29	22	AA187619	Human peptide #606
44	31	68.9	53	22	AA187619	Human peptide #606
45	31	68.9	53	22	AA187619	Peptide #633 encod

#### ALIGNMENTS

RESULT 1

AA187609  
ID AA187609 standard; peptide; 8 AA.

AC AA187609;

XX 21-JUL-2000 (first entry)

DT 21-JUL-2000 (first entry)

XX Murine G protein-coupled receptor antagonist peptide PCP-8.

DE G protein-coupled receptor; antagonist; juxtamembrane; analgesic;  
KW extracellular structural element; intracellular signal transduction;  
KW gynecological; premature delivery; fetus; dysmenorrhea.

XX Synthetic.

OS Synthetic.

XX WO200017348-A1.

XX 30-MAR-2000.

XX 15-SEP-1999; 99WO-CA00844.

XX 17-SEP-1998; 98US-0154627.

XX (HOPI-) HOPITAL SAINTE-JUSTINE.

XX Chemtob S, Peri KG;

XX WPI; 2000-283576/24.

XX New G protein-coupled receptor (GPCR) agonist or antagonist for  
PT preventing premature delivery of fetus and for preventing and/or  
PT treating dysmenorrhea -  
XX

PS Claim 6; Page 30; 37pp; English.

XX This invention describes novel G protein-coupled receptor agonists or

CC antagonists which specifically bind to the juxtamembrane extracellular

CC structural elements of the G protein-coupled receptor in a manner

CC different from that of the natural ligand and where the agonist or

CC antagonist alters the transduction of an intracellular signal. The

CC products of the invention have gynecological and analgesic activity. The

CC G protein-coupled receptor antagonist or its functional derivatives is

CC useful for preventing premature delivery of fetus, and for preventing

CC and/or treating dysmenorrhea. AA87609-Y87620 represent G

CC protein-coupled receptor antagonist peptide fragments which are described

CC in the method of the invention.

XX Sequence 8 AA;

SQ

Query Match 100.0%; Score 45; DB 21; Length 8;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8

Db 1 ILGHRDYK 8

RESULT 2

AA869546

ID AAR69546 standard; Protein; 359 AA.

AC AAR69546;

XX

DT 05-SEP-1995 (first entry)

XX

DE Prostaglandin FP receptor protein.

XX

XX Prostaglandin F2-alpha; PGF2-alpha; FP receptor;

KW activity modulators; glaucoma; oestrus cycle.

KW

XX Homo sapiens.

OS

XX WO9500551-A.

PN

XX 05-JAN-1995.

PD

XX

XX 09-JUN-1994; 94WO-CA00319.

PF

XX

PR 25-JUN-1993; 93US-0083741.

XX

XX (MERI ) MERCK FROSST CANADA INC.

PA

XX Abramovitz M, Grygorczyk R, Metters K, Nguyen T;

PI Rushmore TH, Slipetz D;

PI

XX WPI; 1995-052011/07.

DR

DR N-PSDB; AAQ81959.

XX

XX New prostaglandin FP receptor and DNA - used partic. to identify

PT modulators of prostaglandin receptor activity for treatment of

PT diseases.

PT

XX

PS Claim 2; Page 33; 46pp; English.

XX

XX AAQ81959 encodes AAR69546 the prostaglandin (PG) FP receptor, to

CC which PGF2-alpha binds. The protein can be used to identify

CC modulators of PG receptor activity (claimed), useful in the

CC treatment of PG-related diseases. Selective agonists of the

CC FP receptor may be used to treat glaucoma or to synchronise

CC oestrus cycles in farm animals

XX

XX Sequence 359 AA;

SQ

Query Match 100.0%; Score 45; DB 16; Length 359;

Best Local Similarity 100.0%; Pred. No. 0.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8

Db 1 ILGHRDYK 178

RESULT 4

AA879542

ID AAR79542 standard; Protein; 362 AA.

XX

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8

Db 171 ILGHRDYK 178

RESULT 3

AA83410

ID AAY83410 standard; Protein; 359 AA.

XX

AC AAY83410;

XX

DT 25-SEP-2000 (first entry)

XX

XX Human FP prostaglandin.

DE

XX Prostaglandin; receptor; pulmonary system; glaucoma;

KW identification; allele; polymorphism; detection; prostanoid; FP;

KW IP; DP; EP; TP; human.

KW

XX Homo sapiens.

OS

XX WO200029614-A1.

PN

XX 25-MAY-2000.

PD

XX

XX 12-NOV-1998; 98WO-IB01803.

PF

XX

PR 12-NOV-1998; 98WO-IB01803.

FR

XX (EURO-) EURONA MEDICAL AB.

PA

XX Jonsson L, Lindstroem HR;

PI

XX WPI; 2000-387820/33.

DR

DR N-PSDB; AAZ93893.

XX

XX Assessing prostanoid response status in an individual suffering from

PT prostaglandin associated diseases such as pulmonary hypertension,

PT glaucoma or arteriosclerosis, comprises comparing polymorphic patterns

PT

XX Claim 18; Fig 1; 57pp; English.

PS

XX The prostaglandin receptor family encompasses at least five classes

CC of receptors designated FP, EP, IP, DP and TP receptors which are

CC classified based on their sensitivity to the five primary prostanoids

CC (F2alpha, E2, I2, D2 and TXA2). EP receptors further comprise

CC four subtypes, designated EPI-4, which differ in their responses to

CC various agonists and antagonists. The receptors have also shown a

CC degree of cross reactivity. They may derive from a common ancestral

CC gene. All of the receptors may exist as allelic variants and these

CC polymorphisms may have an affect on a patients reaction to

CC prostanoids. Detection of these polymorphisms may identify patients

CC at risk from toxic or abnormal responses to prostanoid treatment.

CC The prostaglandins play a role in the pulmonary system and in

CC glaucoma.

CC

XX Sequence 359 AA;

SQ

Query Match 100.0%; Score 45; DB 21; Length 359;

Best Local Similarity 100.0%; Pred. No. 0.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8

Db 171 ILGHRDYK 178

RESULT 4

AA879542

ID AAR79542 standard; Protein; 362 AA.

XX

AC AAR79542;  
XX  
DT 12-MAR-1996 (first entry)  
XX  
DE Bovine prostaglandin F2 alpha receptor.  
XX  
KW Bovine; prostaglandin; F2 alpha receptor; corpus luteum; involute;  
KW progesterone; production inhibition.  
XX  
OS Bos taurus.  
XX  
PN JP07135979-A.  
XX  
PD 30-MAY-1995.  
XX  
PF 22-NOV-1993; 93JP-0291796.  
XX  
PR 22-NOV-1993; 93JP-0291796.  
XX  
PA (OSAB-) ZH OSAKA BIOSCIENCE KENKYUSHO.  
XX  
DR WPI; 1995-227400/30.  
DR N-PSDB; AAQ97766.  
XX  
PT Bovine prostaglandin (PG) F2 alpha receptor - reacts directly with  
PT corpus luteum to inhibit progesterone production  
XX  
PS Claim 1; Figs 1-2; 9pp; Japanese.  
XX  
CC AAQ97766 encodes AAR79542 bovine prostaglandin F2 alpha receptor. The  
CC receptor reacts directly with the corpus luteum to inhibit  
CC progesterone prodn., and to involute the corpus luteum.  
XX  
SQ Sequence 362 AA;  
  
Query Match 100.0%; Score 45; DB 16; Length 362;  
Best Local Similarity 100.0%; Pred. NO. 0.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ILGHRDYK 8  
DB 171 ILGHRDYK 178  
  
RESULT 5  
AAY87614  
ID AAY87614 standard; peptide; 8 AA.  
XX  
AC AAY87614;  
XX  
DT 21-JUL-2000 (first entry)  
XX  
DE Murine G protein-coupled receptor antagonist peptide PCP-13.13.  
XX  
KW G protein-coupled receptor; antagonist; juxtamembrane; analgesic;  
KW extracellular structural element; intracellular signal transduction;  
KW gynecological; premature delivery; fetus; dysmenorrhea.  
XX  
OS Synthetic.  
XX  
PN WO200017348-A1.  
XX  
PD 30-MAR-2000.  
XX  
PF 15-SEP-1999; 99WO-CA00844.  
XX  
PR 17-SEP-1998; 98US-0154627.  
XX  
PA (HOPI-) HOPITAL SAINTE-JUSTINE.  
XX  
PI Chemtob S, Peri KG;  
XX  
DR WPI; 2000-283576/24.

XX New G protein-coupled receptor (GPCR) agonist or antagonist for  
PT preventing premature delivery of fetus and for preventing and/or  
PT treating dysmenorrhea -  
XX  
PS Claim 6; Page 31; 37pp; English.  
XX  
CC This invention describes novel G protein-coupled receptor agonists or  
CC antagonists which specifically bind to the juxtamembrane extracellular  
CC structural elements of the G protein-coupled receptor in a manner  
CC different from that of the natural ligand and where the agonist or  
CC antagonist alters the transduction of an intracellular signal. The  
CC products of the invention have gynecological and analgesic activity. The  
CC G protein-coupled receptor antagonist or its functional derivatives is  
CC useful for preventing premature delivery of fetus, and for preventing  
CC and/or treating dysmenorrhea. AAY87609-Y87620 represent G  
CC protein-coupled receptor antagonist peptide fragments which are described  
CC in the method of the invention.  
XX  
SQ Sequence 8 AA;  
  
Query Match 93.3%; Score 42; DB 21; Length 8;  
Best Local Similarity 87.5%; Pred. NO. 6.4e+05;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ILGHRDYK 8  
DB 1 ILGHKDYK 8  
  
RESULT 6  
AAY87616  
ID AAY87616 standard; peptide; 8 AA.  
XX  
AC AAY87616;  
XX  
DT 21-JUL-2000 (first entry)  
XX  
DE Murine G protein-coupled receptor antagonist peptide PCP-13.18.  
XX  
KW G protein-coupled receptor; antagonist; juxtamembrane; analgesic;  
KW extracellular structural element; intracellular signal transduction;  
KW gynecological; premature delivery; fetus; dysmenorrhea.  
XX  
OS Synthetic.  
XX  
PN WO200017348-A1.  
XX  
PD 30-MAR-2000.  
XX  
PF 15-SEP-1999; 99WO-CA00844.  
XX  
PR 17-SEP-1998; 98US-0154627.  
XX  
PA (HOPI-) HOPITAL SAINTE-JUSTINE.  
XX  
PI Chemtob S, Peri KG;  
XX  
DR WPI; 2000-283576/24.  
  
XX New G protein-coupled receptor (GPCR) agonist or antagonist for  
PT preventing premature delivery of fetus and for preventing and/or  
PT treating dysmenorrhea -  
XX  
PS Claim 6; Page 31; 37pp; English.  
XX  
CC This invention describes novel G protein-coupled receptor agonists or  
CC antagonists which specifically bind to the juxtamembrane extracellular  
CC structural elements of the G protein-coupled receptor in a manner  
CC different from that of the natural ligand and where the agonist or  
CC antagonist alters the transduction of an intracellular signal. The  
CC products of the invention have gynecological and analgesic activity. The  
CC G protein-coupled receptor antagonist or its functional derivatives is

CC useful for preventing premature delivery of fetus, and for preventing  
 CC and/or treating dysmenorrhea. AAY87609-Y87620 represent G  
 CC protein-coupled receptor antagonist peptide fragments which are described  
 CC in the method of the invention.

XX SQ Sequence 8 AA;

Query Match 91.1%; Score 41; DB 21; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 6.4e+05;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
 |||||  
 Db 1 ILGHQDYK 8

RESULT 7

AAR79918  
 ID AAR79918 standard; Protein; 366 AA.

XX AC AAR79918;

XX DT 10-MAY-1996 (first entry)

XX DE Mouse prostaglandin-F receptor.

XX KW Prostaglandin-F; receptor; PGF 2-alpha; hypertension; diarrhoea;  
 XX KW asthma; premature birth.

XX OS Mus sp.

XX FN JP07238094-A.

XX PD 12-SEP-1995.

XX FF 24-FEB-1994; 94JP-0051313.

XX PR 24-FEB-1994; 94JP-0051313.

XX PA (ONOOY ) ONO PHARM CO LTD.

XX DR WPI; 1995-348351/45.

XX DR N-PSDB; AAT04098.

XX PT Mammalian prostaglandin F receptor and DNA encoding it - used to  
 PT treat conditions caused by over production of PGF 2-alpha, e.g.

XX PT hypertension and premature birth

XX PS Claim 3; Page 6-7; 11pp; Japanese.

XX CC This sequence is the mouse prostaglandin F receptor (PGFR). cDNA  
 CC encoding the receptor or a fragment of the receptor can be used to  
 CC produce a recombinant PGFR. The PGF polypeptide can be used as a  
 CC preventive and treating agent for diseases and conditions caused by  
 CC over-production of PGF 2-alpha e.g. hypertension, asthma, diarrhoea  
 CC and premature birth.

XX SQ Sequence 366 AA;

Query Match 91.1%; Score 41; DB 16; Length 366;  
 Best Local Similarity 87.5%; Pred. No. 2.7;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
 |||||  
 Db 171 ILGHRDYQ 178

RESULT 8

AAY87617

ID AAY87617 standard; peptide; 7 AA.

XX AC AAY87617;

XX DT 21-JUL-2000 (first entry)

XX DE Murine G protein-coupled receptor antagonist peptide PCP-13.20.

XX KW G protein-coupled receptor; antagonist; juxtamembrane; analgesic;  
 KW extracellular structural element; intracellular signal transduction;  
 KW gynecological; premature delivery; fetus; dysmenorrhea.

XX OS Synthetic.

XX PN WO200017348-A1.

XX PD 30-MAR-2000.

XX PF 15-SEP-1999; 99WO-CA00844.

XX PR 17-SEP-1998; 98US-0154627.

XX PA (HOPI-) HOPITAL SAINTE-JUSTINE.

XX PI Chemtob S, Peri KG;

XX DR WPI; 2000-283576/24.

XX PT New G protein-coupled receptor (GPCR) agonist or antagonist for  
 PT preventing premature delivery of fetus and for preventing and/or  
 PT treating dysmenorrhea.

XX PS Claim 6; Page 31; 37pp; English.

XX CC This invention describes novel G protein-coupled receptor agonists or  
 CC antagonists which specifically bind to the juxtamembrane extracellular  
 CC structural elements of the G protein-coupled receptor in a manner  
 CC different from that of the natural ligand and where the agonist or  
 CC antagonist alters the transduction of an intracellular signal. The  
 CC products of the invention have gynecological and analgesic activity. The  
 CC G protein-coupled receptor antagonist or its functional derivatives is  
 CC useful for preventing premature delivery of fetus, and for preventing  
 CC and/or treating dysmenorrhea. AAY87609-Y87620 represent G  
 CC protein-coupled receptor antagonist peptide fragments which are described  
 CC in the method of the invention.

XX SQ Sequence 7 AA;

Query Match 88.9%; Score 40; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDY 7  
 |||||  
 Db 1 ILGHRDY 7

RESULT 9

AAY87615

ID AAY87615 standard; peptide; 8 AA.

XX AC AAY87615;

XX DT 21-JUL-2000 (first entry)

XX DE Murine G protein-coupled receptor antagonist peptide PCP-13.14.

XX KW G protein-coupled receptor; antagonist; juxtamembrane; analgesic;  
 KW extracellular structural element; intracellular signal transduction;  
 KW gynecological; premature delivery; fetus; dysmenorrhea.

XX OS Synthetic.

XX PN WO200017348-A1.

XX PD 30-MAR-2000.



in mature testis and participate in the differentiation and maturation of sperm. The proteases are potentially useful for the development of pharmaceuticals for the treatment of male infertility and other male reproductive disorders, and for the development of contraceptives. They may also be used as reagents for the diagnosis of male infertility.

Query Match	82.2%	Score 37;	DB 21;	Length 319;
Best Local Similarity	75.0%	Pred. No. 16;		
Matches	6;	Conservative	1;	Mismatches 1;
				Indels 0;
				Gaps 0;

Qy	1	ILGHRDYK	8
		:	
Db	116	IAHRDYK	123

RESULT 12	
AAAY87613	
ID	AAAY87613 standard; peptide; 8 AA.
XX	
XX	AAAY87613;
XX	
XX	
DT	21-JUL-2000 (first entry)
XX	
DE	Murine G protein-coupled receptor antagonist peptide PCP-13.11.
XX	
KW	G protein-coupled receptor; antagonist; juxtamembrane; analgesic;
KW	extracellular structural element; intracellular signal transduction;
KW	gynecological; premature delivery; fetus; dysmenorrhea.
XX	
OS	Synthetic.

PN	WO2000017348-A1.
XX	
XX	30-MAR-2000.
XX	
XX	15-SEP-1999; 99WO-CA00844.
XX	
XX	17-SEP-1998; 98US-0154627.
XX	
XX	(HOPI-) HOPITAL SAINTE-JUSTINE.
XX	
XX	Chemtob S, Peri KG;
XX	
XX	WPI; 2000-283576/24.
XX	
XX	
XX	
PT	New G protein-coupled receptor (GPCR) agonist or antagonist for
PT	preventing premature delivery of fetus and for preventing and/or
PT	treating dysmenorrhea -
XX	
XX	Claim 6; Page 31; 37pp; English.
PS	

This invention describes novel G protein-coupled receptor agonists or antagonists which specifically bind to the juxtamembrane extracellular structural elements of the G protein-coupled receptor in a manner different from that of the natural ligand and where the agonist or antagonist alters the transduction of an intracellular signal. The products of the invention have gynecological and analgesic activity. The G protein-coupled receptor antagonist or its functional derivatives is useful for preventing premature delivery of fetus, and for preventing and/or treating dysmenorrhea. AY87609-Y87620 represent G protein-coupled receptor antagonist peptide fragments which are described in the method of the invention.

```

SQ      Sequence      8 AA;

Query Match      80.0%:      Score 36:      DB 21:      Length 8;
Best Local Similarity      87.5%:      Pred. No. 6.4e+05;
Matches 7:      Conservative      0;      Mismatches      1;      Indels      0;      Gaps      0;

QY      1 ILGHRDYK 8
      ||| ||||

```

1 ILGFRDYK 8

RESULT 13  
AAY87619  
ID AAY87619 standard; peptide; 8 AA.  
XX  
XX AAY87619;  
XX  
XX 21-JUL-2000 (first entry)  
XX  
XX Murine G protein-coupled receptor antagonist peptide PCP-13.24.  
XX  
XX G protein-coupled receptor; antagonist; juxtamembrane; analgesic;  
KW extracellular structural element; intracellular signal transduction;  
KW gynecological; premature delivery; fetus; dysmenorrhea.  
XX  
XX Synthetic.  
OS  
XX WO200017348-A1.  
PN  
XX  
XX 30-MAR-2000.  
PD  
XX  
XX 15-SEP-1999; 99WO-CA00844.  
PF  
XX  
XX 17-SEP-1998; 98US-0154627.  
PR  
XX  
XX (HOPI-) HOPITAL SAINTE-JUSTINE.  
PA  
XX  
XX Chemtob S, Peri KG;  
PI  
XX  
XX WPI; 2000-283576/24.  
DR  
XX  
XX New G protein-coupled receptor (GPCR) agonist or antagonist for  
PT preventing premature delivery of fetus and for preventing and/or  
PT treating dysmenorrhea -  
PT  
XX  
XX Claim 6; Page 32; 37pp; English.  
PS  
XX  
XX This invention describes novel G protein-coupled receptor agonists or  
CC antagonists which specifically bind to the juxtamembrane extracellular  
CC structural elements of the G protein-coupled receptor in a manner  
CC different from that of the natural ligand and where the agonist or  
CC antagonist alters the transduction of an intracellular signal. The  
CC products of the invention have gynecological and analgesic activity. The  
CC G protein-coupled receptor antagonist or its functional derivatives is  
CC useful for preventing premature delivery of fetus, and for preventing  
CC and/or treating dysmenorrhea. AAY87609-Y87620 represent G  
CC protein-coupled receptor antagonist peptide fragments which are described  
CC in the method of the invention.

SQ Sequence 8 AA; Query Match 80.0%; Score 36; DB 21; Length 8; Best Local Similarity 87.5%; Pred. No. 6.4e+05; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 1 ILGHRDYK 8  
||| ||||  
Db 1 ILGXRDYK 8

RESULT 14	
RAY87618	
ID	RAY87618 standard; peptide; 8 AA.
XX	
XX	RAY87618;
XX	
XX	21-JUL-2000 (first entry)
XX	
DE	Murine G protein-coupled receptor antagonist peptide PCP-13.22.
XX	
KW	G protein-coupled receptor; antagonist; juxtamembrane; analgesic;



KW extracellular structural element; intracellular signal transduction;  
KW gynecological; premature delivery; fetus; dysmenorrhea.  
OS Synthetic.  
XX  
PN WO200017348-A1.  
XX  
XX 30-MAR-2000.  
XX  
XX 15-SEP-1999; 99WO-CA00844.  
XX  
XX 17-SEP-1998; 98US-0154627.  
XX  
XX (HOPI-) HOPITAL SAINTE-JUSTINE.  
XX  
XX Chemtob S, Peri KG;  
XX WPI; 2000-283576/24.  
DR  
XX  
XX New G protein-coupled receptor (GPCR) agonist or antagonist for  
PT preventing premature delivery of fetus and for preventing and/or  
PT treating dysmenorrhea -  
XX  
XX Claim 6; Page 32; 37pp; English.  
PS  
XX This invention describes novel G protein-coupled receptor agonists or  
CC antagonists which specifically bind to the juxtamembrane extracellular  
CC structural elements of the G protein-coupled receptor in a manner  
CC different from that of the natural ligand and where the agonist or  
CC antagonist alters the transduction of an intracellular signal. The  
CC products of the invention have gynecological and analgesic activity. The  
CC G protein-coupled receptor antagonist or its functional derivatives is  
CC useful for preventing premature delivery of fetus, and for preventing  
CC and/or treating dysmenorrhea. AAY87609-Y87620 represent G  
CC protein-coupled receptor antagonist peptide fragments which are described  
CC in the method of the invention.  
XX  
XX Sequence 8 AA;  
XX  
XX Query Match 77.8%; Score 35; DB 21; Length 8;  
XX Best Local Similarity 87.5%; Pred. No. 6.4e+05;  
XX Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
Qy 1 ILGHRDYK 8  
Db ||| ||||  
1 ILGWRDYK 8  
XX  
RESULT 15  
AAG00735  
ID AAG00735 standard; Protein; 131 AA.  
XX  
AC AAG00735;  
XX  
XX 06-OCT-2000 (first entry)  
XX  
XX Human secreted protein, SEQ ID NO: 4816.  
XX  
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping.  
XX  
XX Homo sapiens.  
XX  
XX EP1033401-A2.  
XX  
XX 06-SEP-2000.  
XX  
XX 21-FEB-2000; 2000EP-0200610.  
XX  
XX 26-FEB-1999; 99US-0122487.  
XX  
XX (GEST ) GENSET.  
XX

PI Dumas Milne Edwards J, Duclert A, Giordano J;  
XX WPI; 2000-500381/45.  
DR N-PSDB; AAC00741.  
DR  
XX  
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
XX  
XX Claim 13; SEQ ID 4816; 71pp + CD-ROM; English.  
XX  
XX The present sequence is a polypeptide encoded by one of a large number  
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs  
CC were prepared from total human RNAs or polyA+ RNAs derived from 30  
CC different tissues. EST sequences usually correspond mainly to the 3'  
CC untranslated region (UTR) of the mRNA because they are often obtained  
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for  
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in  
CC those cases where longer cDNA sequences have been obtained, the full 5'  
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'  
CC ends and can therefore be used to obtain full length cDNAs and genomic  
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and  
CC chromosome mapping procedures. They are used to obtain upstream  
CC regulatory sequences and to design expression and secretion vectors.  
XX  
XX SQ Sequence 131 AA;  
XX  
XX Query Match 77.8%; Score 35; DB 21; Length 131;  
XX Best Local Similarity 75.0%; Pred. No. 15;  
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
XX  
Qy 1 ILGHRDYK 8  
Db :| |||||  
48 LLRRDYK 55  
XX  
Search completed: October 11, 2002, 14:45:51  
Job time : 32 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:42:04 ; Search time 27 seconds  
(without alignments)  
51.258 Million cell updates/sec

Title: US-09-787-334-1  
Perfect score: 45  
Sequence: 1 ILGHRDYK 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	45	100.0	156	6 Q9TR24	Q9tr24 macaca fasc
2	45	100.0	266	4 Q9P1X4	Q9p1x4 homo sapien
3	45	100.0	295	6 Q95W06	Q95m06 bos taurus
4	45	100.0	362	6 Q95L06	Q95l06 sus scrofa
5	41	91.1	366	11 Q9B627	Q9b627 mus musculu
6	38	84.4	102	1 O07119	O07119 halobacteri
7	38	84.4	432	17 Q58874	Q58874 methanococc
8	38	84.4	513	17 Q9HN83	Q9hn83 halobacteri
9	37	82.2	222	11 Q9DAL4	Q9dal4 mus musculu
10	37	82.2	304	16 Q9KNP6	Q9knp6 vibrio chol
11	35	77.8	199	4 Q96NC0	Q96nc0 homo sapien
12	35	77.8	199	11 Q9CPW7	Q9cpw7 mus musculu
13	35	77.8	406	3 Q9Y714	Q9y714 schizosacch
14	35	77.8	530	10 Q82266	Q82266 arabidopsis
15	35	77.8	626	10 Q9SY72	Q9sy72 arabidopsis
16	35	77.8	785	2 Q9K3N5	Q9k3n5 streptomyce

17	34	75.6	121	11 Q61607	Q61607 mus musculu
18	34	75.6	151	16 Q915J2	Q915j2 pseudomonas
19	34	75.6	246	17 Q9HLM5	Q9hlm5 thermoplas
20	34	75.6	246	17 Q978J8	Q978j8 thermoplas
21	34	75.6	487	2 Q30651	Q30651 vibrio chol
22	34	75.6	487	16 Q9KP49	Q9kpd9 vibrio chol
23	34	75.6	489	2 Q24775	Q24775 vibrio algi
24	34	75.6	491	2 Q9KI09	Q9kig9 vibrio harv
25	34	75.6	579	5 Q9W454	Q9w454 drosophila
26	33	73.3	172	16 Q92AS2	Q92as2 listeria in
27	33	73.3	201	5 Q9U8Q7	Q9u8q7 ptychodera
28	33	73.3	267	16 Q98Q26	Q98q26 mycoplasma
29	33	73.3	314	10 Q43863	Q43863 zea mays (m
30	33	73.3	381	10 Q9ASC1	Q9asc1 oryza sativ
31	33	73.3	422	16 Q9WJ0	Q9wj0 staphylococ
32	33	73.3	428	16 Q9PTJ4	Q9ptj4 staphylococ
33	33	73.3	544	16 Q9PAP6	Q9pap6 xylella fas
34	33	73.3	892	11 Q62744	Q62744 rattus norv
35	33	73.3	1131	12 Q56282	Q56282 human herpe
36	32	71.1	74	12 Q9YLX5	Q9ylx5 tt virus. o
37	32	71.1	84	16 Q9WK8	Q9wk8 staphylococ
38	32	71.1	98	16 Q9K9N6	Q9k9n6 bacillus ha
39	32	71.1	104	2 Q9RND9	Q9rnd9 bordetella
40	32	71.1	125	2 Q56642	Q56642 vibrio chol
41	32	71.1	180	16 Q9PAL1	Q9pal1 xylella fas
42	32	71.1	214	3 Q9HEZ5	Q9hez5 neurospora
43	32	71.1	217	16 Q5172	Q5172 synecocyst
44	32	71.1	222	16 Q9XIV6	Q9xlv6 thermotoga
45	32	71.1	231	2 Q93H45	Q93h45 streptomyce

## ALIGNMENTS

## RESULT 1

Q9TR24 ID Q9TR24 PRELIMINARY; PRT; 156 AA.  
AC Q9TR24;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE PROTAGLANDIN F2 ALPHA RECEPTOR (FRAGMENT).  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96181430; PubMed=8603857;  
RA Ocklind A., Lake S., Wentzel P., Nister M., Stjernschantz J.;  
RT "Localization of the prostaglandin F2 alpha receptor messenger RNA and protein in the cynomolgus monkey eye."  
RL Invest. Ophthalmol. Vis. Sci. 37:716-726(1996).  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECP\_FL\_1; UNKNOWN\_1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECP\_FL\_2; 1.  
SQ SEQUENCE 156 AA; 17339 MW; 343DE0150FCFE8AA CRC64;

Query Match 100.0%; Score 45; DB 6; Length 156;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
| | | | | | | |  
Db 139 ILGHRDYK 146

RESULT 2  
Q9P1X4 ID Q9P1X4 PRELIMINARY; PRT; 266 AA.  
AC Q9P1X4;

```
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PROTAGLANDIN F2ALPHA RECEPTOR (FRAGMENT).
GN FP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Nishizawa M., Ito S.;
RL "Structure of human prostaglandin F2alpha receptor gene.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041713; BA94756.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 266 266
      266 AA; 29816 MW; BF12B730760373EC CRC64;

Query Match 100.0%; Score 45; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8
    |||||
Db 171 ILGHRDYK 178

RESULT 3
Q95M06 PRELIMINARY; PRT; 295 AA.
AC Q95M06;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PROTAGLANDIN F2ALPHA RECEPTOR FFA ISOFORM.
GN BFA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Bovidae; Artiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORPUS LUTEUM;
RA Sakamoto K., Ishi Y., Onodera T.;
RL "The novel isoform of bovine prostaglandin F2 alpha receptor.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB061544; BAB71719.1; -.
KW Receptor.
SQ SEQUENCE 295 AA; 33677 MW; 4DCD47314A757F92 CRC64;

Query Match 100.0%; Score 45; DB 6; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8
    |||||
Db 171 ILGHRDYK 178

RESULT 4
Q95L06 PRELIMINARY; PRT; 362 AA.
AC Q95L06;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PROTAGLANDIN F2-ALPHA RECEPTOR.
GN FP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Boonyaparakob U., Gadsby J.E., Hedgpeth V., Routh P., Almond G.W.;
RL "Cloning of an FP receptor from the porcine corpus luteum.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY043485; AAK95379.1; -.
KW Receptor.
SQ SEQUENCE 362 AA; 40724 MW; 9D570C5449C65FE4 CRC64;

Query Match 100.0%; Score 45; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8
    |||||
Db 171 ILGHRDYK 178

RESULT 5
Q9D627 PRELIMINARY; PRT; 366 AA.
AC Q9D627;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PROTAGLANDIN F RECEPTOR.
GN PTGFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HEAD;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK014673; BAB29498.1; -.
DR MGD; MGI:97796; Ptgr.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 366 AA; 40642 MW; 75E7C5F70081FEF0 CRC64;

Query Match 91.1%; Score 41; DB 11; Length 366;
Best Local Similarity 87.5%; Pred. No. 3.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 ILGHRDYK 8  
| | | | |  
Db 171 ILGHRDYQ 178

## RESULT 6

ID O07119 PRELIMINARY; PRT; 102 AA.  
AC O07119;  
DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
DT 01-AUG-1998 (T-EMBLrel. 07, Last annotation update)  
DE PUTATIVE TRYPTOPHANYL AMINOACYL TRNA SYNTHETASE (FRAGMENT).  
TRPS.  
GN Halobacterium volcanii (Haloflex volcanii).  
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloferax.  
OX NCBI\_TaxID=2246;  
RN [1]  
RP MEDLINE=97344075; PubMed=9200602;  
RX Klemm-Leyer K., Armbruster D.W., Daniels C.J.;  
RA "Properties of H. volcanii tRNA intron endonuclease reveal a  
RT relationship between the archaeal and eucaryal tRNA intron processing  
RT systems";  
RL Cell 89:839-847(1997).  
KW EMBL; AF001578; AAC45447.1; -.  
DR Aminoacyl-tRNA synthetase.  
FT NON\_TER 102 102  
SQ SEQUENCE 102 AA; 11442 MW; 56A8D2BA730D6D14 CRC64;

Query Match 84.4%; Score 38; DB 1; Length 102;  
Best Local Similarity 75.0%; Pred. No. 2.9;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8  
| | | | |  
Db 67 IFGHRDYR 74

## RESULT 7

ID Q58874 PRELIMINARY; PRT; 432 AA.  
AC Q58874;  
DT 01-AUG-1998 (T-EMBLrel. 07, Created)  
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL PROTEIN MJ1479.  
GN MJ1479.  
OS Methanococcus jannaschii.  
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;  
OC Methanococcus.  
OX NCBI\_TaxID=2190;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
RX MEDLINE=96337999; PubMed=8688087;  
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,  
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus  
RT jannaschii";  
RL Science 273:1058-1073(1996).  
CC -1- SIMILARITY: TO E.COLI HYPOTHETICAL 45.5 KDA PROTEIN IN LRHA  
CC 3'REGION, H.INFLUENZAE HI0286 AND M.TUBERCULOSIS MTCY279.04C.  
DR EMBL; U67589; AAB99491.1; -.  
DR TIGR; MJ1479; -.  
DR InterPro; IPR001511; AminoTran\_1.  
DR InterPro; IPR000529; Ribosomal\_S6.

DR Pfam; PF00155; aminotran\_1\_2; 1.  
DR PROSITE; PS01048; RIBOSOMAL\_S6; UNKNOWN\_1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 432 AA; 49429 MW; 14D1602E32DB31FE CRC64;

Query Match 84.4%; Score 38; DB 17; Length 432;  
Best Local Similarity 75.0%; Pred. No. 15;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8  
| | | | |  
Db 294 IMGHRNYK 301

## RESULT 8

Q9HN83 PRELIMINARY; PRT; 513 AA.  
AC Q9HN83;  
DT 01-MAR-2001 (T-EMBLrel. 16, Created)  
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)  
DE TRYPTOPHANYL-TRNA SYNTHETASE.  
GN TRPS1 OR VNGZ208G.  
OS Halobacterium sp. (strain NRC-1).  
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;  
OC Halobacterium.  
OX NCBI\_TaxID=64091;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20504483; PubMed=11016950;  
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
RA Shukla H.D., Lasky S.R., Ballig N.S., Thorsson V., Sbrogna J.,  
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,  
RA Leitbauer B., Keller K., Cruz R., Danson M.J., Hough D.W., Dale H.,  
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Jung K.-H.,  
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudis J.L., Omer A.D.,  
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;  
RT "Genome sequence of Halobacterium species NRC-1";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
DR EMBL; AE005107; AAC20338.1; -.  
DR InterPro; IPR002305; tRNA-synt\_1b.  
DR InterPro; IPR002306; tRNA-synt\_trp.  
DR Pfam; PF00579; tRNA-synt\_1b; 1.  
DR PRINTS; PR01039; TRNASYNTHTRP.  
KW Aminoacyl-tRNA synthetase; Complete proteome.  
SQ SEQUENCE 513 AA; 56055 MW; 56C06025F3E502B CRC64;

Query Match 84.4%; Score 38; DB 17; Length 513;  
Best Local Similarity 75.0%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8  
| | | | |  
Db 59 IFGHRDYR 66

## RESULT 9

Q9DAL4 PRELIMINARY; PRT; 222 AA.  
AC Q9DAL4;  
DT 01-JUN-2001 (T-EMBLrel. 17, Created)  
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
DE 1700007N14RIK PROTEIN.  
GN 1700007N14RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=TESTIS;

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RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
DR EMBL: AK005740; BAB24215.1; -.
DR HSSP; P20231; IAAO.
DR MGD; MGI:1921465; 1700007W14RIK.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Trypsin.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PF00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP-SFC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR KJ000000; Serine protease.
KW Hydrolyase: Serine protease.
SQ SEQUENCE 222 AA; 24970 MW; 302569496D7CA553 CRC64;

Query Match 82.2%; Score 37; DB 11; Length 222;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8
: | | | | |
Db 19 IIAHRDYK 26

RESULT 10
Q9KNP6 PRELIMINARY; PRT; 304 AA.
AC Q9KNP6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 5,10-METHYLENETETRAHYDROFOLATE REDUCTASE.
GN VC2685.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=686;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.N.;
RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
DR EMBL; AE004334; AAF95826.1; -.
DR HSSP; P00394; 1B5T.
DR TIGR; VC2685; -.

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DR InterPro; IPR003171; Methetetrhydrof_redctse.
DR Pfam; PF02219; MTHFR; 1.
KW Complete proteome.
SQ SEQUENCE 304 AA; 33956 MW; D87020F874707D8 CRC64;

Query Match 82.2%; Score 37; DB 16; Length 304;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LGHRDYK 8
: | | | | |
Db 3 LGHREYK 9

RESULT 11
Q96NC0 PRELIMINARY; PRT; 199 AA.
AC Q96NC0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CDNA FLJ31121 FIS, CLONE IMR322000742, WEAKLY SIMILAR TO HYPOTHETICAL
DE ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK055683; BAB70983.1; -.
SQ SEQUENCE 199 AA; 23612 MW; EF419358B7977E36 CRC64;

Query Match 77.8%; Score 35; DB 4; Length 199;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8
: | | | | |
Db 48 LLHRDYK 55

RESULT 12
Q9CPW7 PRELIMINARY; PRT; 199 AA.
AC Q9CPW7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 2610510D14RIK PROTEIN.
GN 2610510D14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO, AND STOMACH;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA

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RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Hayashizaki Y.,
RA Yonshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK012091; BAB28023.1; -.
DR EMBL; AK008717; BAB25852.1; -.
DR MGI; MGI:1913742; 2610510D14Rik.
DR InterPro; IPR000822; Znf-C2H2.
DR InterPro; IPR003604; Znf-U1.
DR SMART; SM00355; Znf-C2H2; 1.
DR SMART; SM00451; Znf-U1; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
SQ SEQUENCE 199 AA; 23612 MW; EF419358B7977E36 CRC64;

Query Match 77.8%; Score 35; DB 11; Length 199;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8
Db :|||
48 LLRRDYK 55

RESULT 13
QY714 PRELIMINARY; PRT; 406 AA.
AC QY714;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PUTATIVE MANNOSYLTRANSFERASE C7D4.06C (EC 2.4.1.-).
GN SPAC7D4.06C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Gentles S., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- PATHWAY: GLYCOSYLATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
RETICULUM (BY SIMILARITY).
DR EMBL; Z99532; CAB16723.2; -.
KW Hypothetical protein; Transferase; Glycosyltransferase; Transmembrane;
KW Endoplasmic reticulum.
FT DOMAIN 30 33 POLY-LEU.
FT TRANSMEM 214 234 POTENTIAL.
FT TRANSMEM 261 281 POTENTIAL.
FT TRANSMEM 349 369 POTENTIAL.
SQ SEQUENCE 406 AA; 46991 MW; 039E40A16A9359C8 CRC64;

Query Match 77.8%; Score 35; DB 3; Length 406;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8
Db :|||
63 LLGERDYK 70

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RESULT 14
O82266 PRELIMINARY; PRT; 530 AA.
ID O82266;
AC O82266;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AT2G47990 PROTEIN.
DE AT2G47990.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Arabidopsids II; Brassicales; Brassicaceae; Arabidopsids.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. COLUMBIA;
RC MEDLINE=20083487; PubMed=10617197;
RX Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. COLUMBIA;
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AC005309; AAC63653.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR00320; GPROTEINBRPT.
DR SMART; SM00320; WD40; 5.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS00082; WD_REPEATS_2; 2.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 530 AA; 58903 MW; 6F1B4AB984F3162B CRC64;

Query Match 77.8%; Score 35; DB 10; Length 530;
Best Local Similarity 71.4%; Pred. No. 77;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDY 7
Db :|||
174 LLGHKY 180

RESULT 15
Q9SY72 PRELIMINARY; PRT; 626 AA.
ID Q9SY72;
AC Q9SY72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE F14N23.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP SHINN P., Dunn P., Walker M., Buehler E., Kim C., Altafi H.,
RA Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F., Huizar L.,
RA Kremenetskaia I., Lenz C., Li J., Liu S., Lueros S., Rowley D.,

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RA Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W.,  
RA Federspiel N.A., Theologis A., Ecker J.R.;  
RT "Genomic sequence for Arabidopsis thaliana BAC F14N23 from Chromosome  
1.";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBDJ databases.  
DR EMBL; AC005489; AAD32890.1; -;  
DR InterPro; IPR000765; GTP\_OBG.  
DR PRINTS; PR00326; GTP\_OBG.  
SQ SEQUENCE 626 AA; 71332 MW; 61C7D49D484A61AA CRC64;

Query Match 77.8%; Score 35; DB 10; Length 626;  
Best Local Similarity 85.7%; Pred. No. 94;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LGHRDYK 8  
||| |||  
Db 236 LGHTDYK 242

Search completed: October 11, 2002, 14:46:55  
Job time : 29 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:41:24 ; Search time 11 seconds  
(without alignments)  
28.160 Million cell updates/sec

Title: US-09-787-334-1

Perfect score: 45

Sequence: 1 ILGHRDYK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	45	100.0	359	1 PF2R_HUMAN	P43088 homo sapien
2	45	100.0	362	1 PF2R_BOVIN	P37289 bos taurus
3	45	100.0	362	1 PF2R_SHEEP	Q28905 ovis aries
4	41	91.1	366	1 PF2R_MOUSE	P43117 mus musculus
5	41	91.1	366	1 PF2R_RAT	P43118 rattus norv
6	37	82.2	364	1 SYW_METH	Q26352 methanobact
7	37	82.2	370	1 SYW_METJA	Q58810 methanococc
8	36	80.0	157	1 YBUK_CLOBE	Q05626 clostridium
9	36	80.0	420	1 SYW_ARCFU	O28579 archaeoglob
10	36	80.0	486	1 RP54_VIBAN	O08429 vibrio angu
11	35	77.8	354	1 DCUP_PASMU	P57964 pasteurella
12	34	75.6	380	1 AROC_AERPE	O39414 aeropyrum p
13	33	73.3	87	1 Y253_CAMJE	Q9p1p2 campylobact
14	33	73.3	259	1 Y238_METJA	Q60293 methanococc
15	33	73.3	343	1 E2B_THEMA	O9x013 thermotoga
16	33	73.3	428	1 GSA_STAAU	O34092 staphylococ
17	33	73.3	456	1 FD3_DROME	Q02361 drosophila
18	33	73.3	1131	1 DNBI_HSVJ7	P52339 human herpe
19	32	71.1	245	1 FGF3_MOUSE	P05524 mus musculu
20	32	71.1	374	1 SYW_AERPE	Q9y924 aeropyrum p
21	32	71.1	592	1 RB56_HUMAN	Q92804 homo sapien
22	32	71.1	634	1 NOG1_HUMAN	O9bze4 homo sapien
23	32	71.1	634	1 NOG1_MOUSE	O99me9 mus musculu
24	32	71.1	652	1 NOG1_DROME	Q9v411 drosophila
25	32	71.1	671	1 NOG1_ARATH	Q9c618 arabidopsis
26	32	71.1	868	1 MCM2_YEAST	P29469 saccharomyc
27	32	71.1	923	1 PWP2_YEAST	P25635 saccharomyc
28	32	71.1	959	1 N100_YEAST	Q02629 saccharomyc
29	32	71.1	1739	1 CHD2_HUMAN	O14647 homo sapien
30	32	71.1	1807	1 ITB4_RAT	Q64632 rattus norv
31	31	68.9	141	1 ATPE_MYCPU	Q98q66 mycoplasma
32	31	68.9	231	1 ATMC_SALT	P22037 salmonella
33	31	68.9	231	1 YF07_MYCTU	P71786 mycobacteri

#### RESULT 1

ID	PF2R_HUMAN	STANDARD;	PRT;	359 AA.
AC	P43088; O9PIX4;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Prostaglandin F2-alpha receptor (prostanoid FP receptor) (PGF receptor) (PGF2 alpha receptor).			
GN	PTGFR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Uterus;			
RX	MEDLINE=94132028; PubMed=8300593;			
RA	Abramovitz M., Boie Y., Nguyen T., Rushmore T.H., Bayne M.A.,			
RA	Metters K.M., Slipetz D.M., Grygorczyk R.;			
RT	"Cloning and expression of a cDNA for the human prostanoid FP			
RT	receptor.";			
RL	J. Biol. Chem. 269:2632-2636(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Ocular ciliary body;			
RA	Kunapuli P., Lawson J.A., Hwang S.W., Adiyaman M., Khanapure S.P.,			
RA	Rokach J., Fitzgerald G.A.;			
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Sehra H.;			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE OF 1-266 FROM N.A.			
RC	TISSUE=Liver;			
RA	Nishizawa M., Ito S.;			
RT	"Structure of human prostaglandin F2-alpha receptor gene.";			
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: RECEPTOR FOR PROSTAGLANDIN F2-ALPHA (PGF2-ALPHA). THE			
CC	ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE			
CC	A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. INITIATES			
CC	LUTEOLYSIS IN THE CORPUS LUTEUM (BY SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> ).			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .			
CC	-----			
DR	EMBL; L24470; AAA17684.1; -.			
DR	EMBL; AF004021; AAB63152.1; -.			

O28366 archaeoglob  
P07963 methanococc  
Q58255 methanococc  
P11563 methanococc  
Q00710 emeticella  
Q28234 cervus elap  
Q80916 human papil  
Q80937 human papil  
Q05889 leishmania  
P53973 saccharomyc  
P48423 grosophila  
Q27954 bos taurus

#### ALIGNMENTS

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DR EMBL; AL136324; CAC36038.1; -.
DR EMBL; AB041713; BAA94756.1; -.
DR GCRDB; GCR_0905; -.
DR GCRDB; GCR_2410; -.
DR MIM; 600563; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; -.
DR PRINTS; PR00855; PRSTNOIDFPR.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 32 54 1 (POTENTIAL).
FT DOMAIN 56 69 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 70 90 2 (POTENTIAL).
FT DOMAIN 91 109 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 110 131 3 (POTENTIAL).
FT DOMAIN 132 152 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 153 175 4 (POTENTIAL).
FT DOMAIN 176 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 224 5 (POTENTIAL).
FT DOMAIN 225 250 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 251 267 6 (POTENTIAL).
FT DOMAIN 268 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 307 7 (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 19 19 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 359 AA; 40054 MW; 08077045C0B20BCA CRC64;

Query Match 100.0%; Score 45; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8
Db 171 ILGHRDYK 178

RESULT 2
PF2R_BOVIN STANDARD; PRT; 362 AA.
AC P37289;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prostaglandin F2-alpha receptor (Prostanoid FP receptor) (PGF
DE receptor) (PGF2 alpha receptor).
GN PTGFR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Corpus luteum;
RX MEDLINE=94148901; PubMed=7508922;
RA Sakamoto K., Ezashi T., Miwa K., Okuda-Ashitaka E., Houtani T.,
RA Sugimoto T., Ito S., Hayaishi O.;
RT "Molecular cloning and expression of a cDNA of the bovine
RT prostaglandin F2 alpha receptor.";
RL J. Biol. Chem. 269:3881-3886(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97341070; PubMed=9197544;
RA Ezashi T., Sakamoto K., Miwa K., Okuda-Ashitaka E., Ito S.,
RA Hayaishi O.;
RT "Genomic organization and characterization of the gene encoding
RT bovine prostaglandin F2alpha receptor.";
RL Gene 190:271-278(1997).
```

RC STRAIN=WESTERN RANGE; TISSUE=Corpus luteum;  
 RX MEDLINE=95354592; PubMed=7628379;  
 RA Graves P.E., Pierce K.L., Bailey T.J., Rueda B.R., Gil D.W.,  
 RA Woodward D.F., Yool A.J., Hoyer P.B., Regan J.W.;  
 RT "Cloning of a receptor for prostaglandin F2 alpha from the ovine  
 corpus luteum.";  
 RL Endocrinology 136:3430-3436(1995).  
 [2]  
 RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Corpus luteum;  
 RX MEDLINE=97150841; PubMed=8995377;  
 RA Pierce K.L., Bailey T.J., Hoyer P.B., Gil D.W., Woodward D.F.,  
 RA Regan J.W.;  
 RT "Cloning of a carboxyl-terminal isoform of the prostanoid FP  
 receptor.";  
 RL J. Biol. Chem. 272:883-887(1997).  
 CC -1- FUNCTION: RECEPTOR FOR PROSTAGLANDIN F2-ALPHA (PGF2-ALPHA). THE  
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
 CC A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. INITIATES  
 CC LUTEOLYSIS IN THE CORPUS LUTEUM.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: FP-A (SHOWN HERE) AND FP-B;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. FP-A AND FP-B HAVE IDENTICAL  
 CC LIGAND BINDING PROPERTIES BUT DIFFERENT G PROTEIN COUPLING  
 CC PROPERTIES. FP-B SHOWS AGONIST-INDEPENDENT CONSTITUTIVE ACTIVITY,  
 CC BUT IS STILL RESPONSIVE TO AGONIST.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION IS HIGH IN THE MIDLUTEAL PHASE  
 CC CORPUS LUTEUM AND DECREASES DURING LUTEOLYSIS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 CC EMBL: U73798; AAB51070.1; -;  
 DR GCRDb; GCR\_1579; -;  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00855; PRSTNOIDFPR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 Alternative splicing;  
 FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 32 54 1 (POTENTIAL).  
 FT DOMAIN 56 69 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 70 90 2 (POTENTIAL).  
 FT DOMAIN 91 109 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 110 131 3 (POTENTIAL).  
 FT DOMAIN 132 152 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 153 175 4 (POTENTIAL).  
 FT DOMAIN 176 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 224 5 (POTENTIAL).  
 FT DOMAIN 225 250 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 251 267 6 (POTENTIAL).  
 FT DOMAIN 268 285 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 286 307 7 (POTENTIAL).  
 FT DOMAIN 308 362 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 108 186 BY SIMILARITY.  
 FT VARSPIC 317 362 VCFRCGVHVISLHWELSSIKNSLKVASLDLPVTEKVT  
 FT CONFLICT 6 6 S -> C (IN REF. 2).  
 FT SEQUENCE 362 AA; 40984 MW; 83604FC18EADF583 CRC64;  
 Query Match 100.0%; Score 45; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8  
 Db 171 ILGHRDYK 178  
 RESULT 4  
 PF2R\_MOUSE STANDARD; PRT; 366 AA.  
 ID PF2R\_MOUSE  
 AC P43117;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Prostaglandin F2-alpha receptor (Prostanoid FP receptor) (PGF  
 receptor) (PGF2 alpha receptor).  
 GN PTGFR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DDY; TISSUE=Ovary;  
 RX MEDLINE=94117451; PubMed=8288601;  
 RA Sugimoto Y., Hasumoto K.Y., Namba T., Irie A., Katsuyama M.,  
 RA Negishi M., Kakizuka A., Narumiya S., Ichikawa A.;  
 RT "Cloning and expression of a cDNA for mouse prostaglandin F  
 receptor.";  
 RL J. Biol. Chem. 269:1356-1360(1994).  
 CC -1- FUNCTION: RECEPTOR FOR PROSTAGLANDIN F2-ALPHA (PGF2-ALPHA). THE  
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE  
 CC A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. INITIATES  
 CC LUTEOLYSIS IN THE CORPUS LUTEUM (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL: D17433; BAA04251.1; -;  
 DR GCRDb; GCR\_0965; -;  
 DR MGD; MGI:97796; Ptgfr.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00855; PRSTNOIDFPR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 32 54 1 (POTENTIAL).  
 FT DOMAIN 56 69 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 70 90 2 (POTENTIAL).  
 FT DOMAIN 91 109 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 110 131 3 (POTENTIAL).  
 FT DOMAIN 132 152 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 153 175 4 (POTENTIAL).  
 FT DOMAIN 176 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 224 5 (POTENTIAL).  
 FT DOMAIN 225 250 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 251 267 6 (POTENTIAL).  
 FT DOMAIN 268 285 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 286 307 7 (POTENTIAL).  
 FT DOMAIN 308 366 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 108 186 BY SIMILARITY.  
 FT SEQUENCE 366 AA; 40699 MW; B01CB3B271007582 CRC64;

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Query Match      91.1%; Score 41; DB 1; Length 366;
Best Local Similarity 87.5%; Pred. No. 0.86;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ILGHRDYK 8
Db 171 ILGHRDYQ 178

RESULT 5
PF2R_RAT
ID PF2R_RAT STANDARD; PRT; 366 AA.
AC P43118; 062787;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Prostaglandin F2-alpha receptor (Prostanoid FP receptor) (PGF
DE receptor) (PGF2 alpha receptor).
GN PTGFR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain cortex;
RX MEDLINE=95063114; PubMed=7972878;
RA Kitanaka J., Hashimoto H., Sugimoto Y., Negishi M., Aino H., Gotoh M.,
RA Ichikawa A., Baba A.;
RT "Cloning and expression of a cDNA for rat prostaglandin F2 alpha
RT receptor.";
RL Prostaglandins 48:31-41(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95080404; PubMed=7988697;
RA Lake S., Gullberg H., Wahlgvist J., Sjoegren A.-M., Kinhult A.,
RA Lind P., Hellstrom-Lindahl E., Stjernschantz J.;
RT "Cloning of the rat and human prostaglandin F2 alpha receptors and
RT the expression of the rat prostaglandin F2 alpha receptor.";
RN FEBS Lett. 355:317-325(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=Liver;
RA de Vries C., Neuschaefer-Rube F., Haenecke K., Jungermann K.,
RA Puschel G.P.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Ovary;
RX MEDLINE=97069830; PubMed=8912810;
RA Olofsson J.I., Leung C.H.B., Bjurulf E., Ohno T., Selstam G., Peng C.,
RA Leung P.C.K.;
RT "Characterization and regulation of a mRNA encoding the prostaglandin
RT F2alpha receptor in the rat ovary.";
RL Mol. Cell. Endocrinol. 123:45-52(1996).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Ovary;
RX MEDLINE=96397016; PubMed=8804121;
RA Orlicky D.J.;
RT "Negative regulatory activity of a prostaglandin F2 alpha receptor
RT associated protein (FPRP).";
RL Prostaglandins Leukot. Essent. Fatty Acids 54:247-259(1996).
CC -1- FUNCTION: RECEPTOR FOR PROSTAGLANDIN F2-ALPHA (PGF2-ALPHA). THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. INITIATES
CC LUTEOLYSIS IN THE CORPUS LUTEUM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN PREGNANT OVARY. ALSO
CC FOUND IN A LOW EXTENT IN THE KIDNEY. IN THE BRAIN, EXPRESSED IN
CC ASTROCYTES AND OLIGODENDROCYTES, AND MENINGEAL FIBROBLASTS, BUT
CC NOT IN MICROGLIA CELLS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL; D28581; BAA05917.1; -;  
CC EMBL; S74898; AAB32739.1; -;  
CC EMBL; X83856; CAA58736.1; -;  
CC EMBL; U47287; AAB47872.1; -;  
CC EMBL; U26663; AAB19233.1; -;  
CC GCRDb; GCR\_1163; -;  
CC GCRDb; GCR\_1421; -;  
CC GCRDb; GCR\_1442; -;  
CC GCRDb; GCR\_1465; -;  
CC GCRDb; GCR\_1495; -;  
CC InterPro; IPR000276; GPCR\_Rhodpsn.  
CC Pfam; PF00001; 7tm.1; 1.  
CC PRINTS; PR00855; PRSTNOIDPR.  
CC PROSITE; PS00237; G\_PROTEIN\_RECIP\_F1\_1; 1.  
CC PROSITE; PS0262; G\_PROTEIN\_RECIP\_F1\_2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein.  
KW DOMAIN 1 31  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 32 54  
FT DOMAIN 56 69  
FT CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 70 90  
FT DOMAIN 91 109  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 110 131  
FT DOMAIN 132 152  
FT CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 153 175  
FT DOMAIN 176 198  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 199 224  
FT DOMAIN 225 250  
FT TRANSMEM 251 267  
FT DOMAIN 268 285  
FT TRANSMEM 286 307  
FT DOMAIN 308 366  
FT CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 4 4  
FT CARBOHYD 19 19  
FT DISULFID 108 186  
FT CONFLICT 10 10  
FT CONFLICT 113 113  
FT CONFLICT 113 113  
SQ SEQUENCE 366 AA; 40654 MW; D44C47F18B326FBA CRC64;  
Query Match 91.1%; Score 41; DB 1; Length 366;  
Best Local Similarity 87.5%; Pred. No. 0.86;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 ILGHRDYK 8  
Db 171 ILGHRDYQ 178  
RESULT 6  
SYW\_METTH  
ID SYW\_METTH STANDARD; PRT; 364 AA.  
AC O26352;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)  
DE (TPRS).  
GN TRPS OR MTH251.  
OS Methanobacterium thermoautotrophicum.  
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;  
OC Methanotermobacter.  
OX NCBI\_TaxID=145262;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DELTA H;

```

RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
CC diphosphate + L-tryptophanyl-tRNA(Trp).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC
CC EMBL; AE000812; AAB84757.1; -
CC InterPro; IPR002305; tRNA-synt_1b.
CC InterPro; IPR001412; tRNA-synt_1.
CC Pfam; PF00579; tRNA-synt_1b; 1.
CC PRINTS; PR01039; TRNASYNTHTRP.
CC PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 70 78 "HIGH" REGION.
FT SITE 251 255 "KMSKS" REGION.
SQ SEQUENCE 364 AA; 41301 MW; C2F348903338F61D CRC64;

Query Match 82.2%; Score 37; DB 1; Length 364;
Best Local Similarity 75.0%; Pred. No. 5.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8
DB 43 IFGHRDYE 50

RESULT 7
SYW_MENJA
ID SYW_METJA STANDARD; PRT; 370 AA.
AC Q56810;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
DE (TPRS).
GN TRPS OR MJ1415.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus

```

```

RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
CC diphosphate + L-tryptophanyl-tRNA(Trp).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC
CC EMBL; U67582; AAB99425.1; -
CC TIGR; MJ1415; -
CC InterPro; IPR002305; tRNA-synt_1b.
CC InterPro; IPR001412; tRNA-synt_1.
CC Pfam; PF00579; tRNA-synt_1b; 1.
CC PRINTS; PR01039; TRNASYNTHTRP.
CC PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT SITE 75 83 "HIGH" REGION.
FT SITE 255 259 "KMSKS" REGION.
SQ SEQUENCE 370 AA; 42660 MW; B6C71107CF82B59D CRC64;

Query Match 82.2%; Score 37; DB 1; Length 370;
Best Local Similarity 75.0%; Pred. No. 5.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8
DB 48 ILGHRDFE 55

RESULT 8
YBUK_CLOBE
ID YBUK_CLOBE STANDARD; PRT; 157 AA.
AC Q05626;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 18.9 kDa protein in buk 3' region (ORF4).
OS Clostridium beijerinckii (Clostridium MP).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1520;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=ATCC 51743 / NCIMB 8052 / NCIB 8052;
RX MEDLINE=93380658; PubMed=8396545;
RA Oultram J.D., Burr I.D., Elmore M.J., Minton N.P.;
RT "Cloning and sequence analysis of the genes encoding
RT phosphotransbutyrylase and butyrate kinase from Clostridium
RL acetobutylicum NCIMB 8052.";
RL Gene 131:107-112(1993).
CC
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CC
CC EMBL; L04468; AAA52082.1; -
CC PIR; JN0796; JN0796.
CC InterPro; IPR002819; HD.
CC InterPro; IPR003607; HDC.
CC Pfam; PF01966; HD; 1.

```

DR SMART; SM00471; Hdc; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 157 AA; 18896 MW; 0A02DFALDEA50910 CRC64;

Query Match 80.0%; Score 36; DB 1; Length 157;  
Best Local Similarity 87.5%; Pred. No. 3.6;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
| | | | | | | |  
Db 110 ILGHRDKK 117

## RESULT 9

SYW\_ARCFU  
ID SYW\_ARCFU STANDARD; PRT; 420 AA.  
AC O28579;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)  
DE (TIPRS).  
GN TRPS OR AF1694.  
OS Archaeoglobus fulgidus.  
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;  
OC Archaeoglobus.  
OX NCBI\_TaxID=2234;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
RX MEDLINE=98049343; PubMed=9389475;  
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,  
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
RA Cotton M.D., Spriggs T., Artiaach P., Kaine B.P., Sykes S.M.,  
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
RA Venter J.C.;  
RT The complete genome sequence of the hyperthermophilic, sulphate-  
reducing archaeon Archaeoglobus fulgidus.";  
RL Nature 390:364-370(1997).  
CC -|- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +  
diphosphate + L-tryptophanyl-tRNA(Trp).  
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -|- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.  
-----  
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-----  
DR EMBL; AE000986; AAB89554.1; -  
DR TIGR; AF1694; -

DR InterPro; IPR002305; tRNA-synt\_lb.  
DR InterPro; IPR001412; tRNA-synt\_i.  
DR InterPro; IPR002306; tRNA-synt\_trp.  
DR Pfam; PF00579; tRNA-synt\_lb; 1.  
DR PRINTS; PR01039; TRNASYNTHTRP.  
DR PROSITE; PS00178; AA-TRNA\_LIGASE\_I; FALSE\_NEG.  
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
KW Complete proteome.  
FT SITE 72 80 "HIGH" REGION.  
FT SITE 308 312 "KMSKS" REGION.  
SQ SEQUENCE 420 AA; 47283 MW; 9315152E2F172F24 CRC64;  
Query Match 80.0%; Score 36; DB 1; Length 420;

Best Local Similarity 85.7%; Pred. No. 9.5;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILGHRDY 7  
| | | | | |  
Db 45 IFGHRDY 51

## RESULT 10

RP54\_VIBAN  
ID RP54\_VIBAN STANDARD; PRT; 486 AA.  
AC O08429;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE RNA polymerase sigma-54 factor.  
GN RPON.  
OS Vibrio anguillarum (Listonella anguillarum).  
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Listonella.  
OX NCBI\_TaxID=55601;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NB10 / SEROTYPE O1;  
RX MEDLINE=98083740; PubMed=9421909;  
RA O'Toole R., Milton D.L., Horstedt P., Wolf-Watz H.;  
RT "RpoN of the fish pathogen Vibrio (Listonella) anguillarum is  
RT essential for flagellum production and virulence by the water-borne  
RT but not intraperitoneal route of inoculation."  
RL Microbiology 143:3849-3859(1997).  
CC -|- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES  
CC ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND  
CC THEN IS RELEASED.  
CC -|- SIMILARITY: BELONGS TO THE SIGMA-54 FACTOR FAMILY.  
-----  
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-----  
DR EMBL; U06585; AAB95223.1; -  
DR InterPro; IPR000394; Sigma54\_factor.  
DR Pfam; PF00309; Sigma54\_factor; 1.  
DR PRINTS; PR00045; SIGMA54FACT.  
DR PROSITE; PS00717; SIGMA54\_1; 1.  
DR PROSITE; PS00718; SIGMA54\_2; 1.  
DR PROSITE; PS00044; SIGMA54\_3; 1.  
KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;  
KW DNA-binding.  
FT DOMAIN 6 21 GLN-RICH.  
FT DNA\_BIND 375 394 H-T-H MOTIF (POTENTIAL).  
FT SITE 463 471 RPON\_BOX.  
SQ SEQUENCE 486 AA; 54641 MW; 966E6E5EBDC4D657 CRC64;

Query Match 80.0%; Score 36; DB 1; Length 486;  
Best Local Similarity 75.0%; Pred. No. 11;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
| | | | | | | |  
Db 237 LLGNRDYK 244

## RESULT 11

DCUP\_PASMU  
ID DCUP\_PASMU STANDARD; PRT; 354 AA.  
AC P57964;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).

```

GN HEME OR UROD OR PM1734.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- CATALYTIC ACTIVITY: Uroporphyrinogen-III - coproporphyrinogen + 4
CO(2).
CC -1- PATHWAY: PORPHYRIN BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.
-----
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-----
DR EMBL; AE006210; AAK03818.1; -.
DR InterPro; IPR000257; Uroporphyrinogen-decarbxylys.
DR Pfam; PF01208; URO-D; 1.
DR PROSITE; PS00906; UROD_1; 1.
DR PROSITE; PS00907; UROD_2; 1.
DR KW Lyase; Decarboxylase; Porphyrin biosynthesis; Complete proteome.
SQ SEQUENCE 354 AA; 39159 MW; 47D99D4C606F7E97 CRC64;

Query Match 77.8%; Score 35; DB 1; Length 354;
Best Local Similarity 71.4%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ILGHRDY 7
:||||:
*Db 213 VLGHREY 219

RESULT 12
ID AROC_AERPE STANDARD; PRT; 380 AA.
AC Q9VEL4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Chorismate synthase (EC 4.6.1.4) (5-enolpyruvylshikimate-3-phosphate
DE phospholyase).
GN AROC OR APE0564.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankaï A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamaya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
CC -1- CATALYTIC ACTIVITY: 5-O-(1-carboxyvinyl)-3-phosphoshikimate -
CC chorismate + phosphate.
CC -1- COFACTOR: REDUCED FLAVIN (BY SIMILARITY).

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CC -1- PATHWAY: SEVENTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE
CC BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC -1- SIMILARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
-----
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-----
DR EMBL; AP000060; BAA79532.1; -.
DR InterPro; IPR000453; Chorismate_synth.
DR Pfam; PF01264; Chorismate_synth; 1.
DR PRODOM; PD002941; Chorismate_synth; 1.
DR PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.
DR PROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.
DR PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.
DR KW Lyase; Aromatic amino acid biosynthesis; Complete proteome.
SQ SEQUENCE 380 AA; 41086 MW; 310F556D7C2C4E2B CRC64;

Query Match 75.6%; Score 34; DB 1; Length 380;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LGHRDYK 8
:||||:
Db 116 LGHQDYR 122

RESULT 13
ID Y253_CAMJE STANDARD; PRT; 87 AA.
AC Q9PIP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein Cj0253.
GN Cj0253.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
CC -1- SIMILARITY: TO H.PYLORI HP0495/JHP0447.
-----
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-----
DR EMBL; AL139074; CAB72721.1; -.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 87 AA; 10328 MW; EE0C32A21C99A2A9 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 87;
Best Local Similarity 75.0%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ILGHRDYK 8
DB 38 ILGQREYK 45

RESULT 14
Y238_METJA
ID Y238_METJA STANDARD; PRT; 259 AA.
AC Q60293;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJEC138.
GN MJEC138
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RL Science 273:1058-1073(1996).
CC -----
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CC -----
DR EMBL; L77118; AAC37107.1; -
DR TIGR; MJEC138; -
DR InterPro; IPR002850; DUF132.
DR Pfam; PF01999; DUF132; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 235 255 POTENTIAL.
FT DOMAIN 123 163 LYS-RICH.
FT DOMAIN 239 255 ILE-RICH.
SQ SEQUENCE 259 AA; 30076 MW; 00AEC07D21973C0A CRC64;

Query Match 73.3%; Score 33; DB 1; Length 259;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8
DB 168 LIGHRDYK 175

RESULT 15
E2B_THEME
ID E2B_THEME STANDARD; PRT; 343 AA.
AC Q9X013;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative translation initiation factor eIF-2B (eIF-2B GDP-GTP exchange
DE factor).
DE TM0911.
GN TM0911
OS Thermotoga maritima.

Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.W., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima."
EL Nature 399:323-329(1999).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF INITIATION FACTOR 2-BOUND GDP
CC FOR GTP (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE EIF-2B ALPHA/BETA/Delta SUBUNITS
CC FAMILY.
CC -----
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CC -----
DR EMBL; AF001755; AAD35992.1; -
DR TIGR; TM0911; -
DR InterPro; IPR000649; IF-2B.
DR Pfam; PF01008; IF-2B; 1.
KW Hypothetical protein; Initiation factor; Protein biosynthesis;
KW Complete proteome.
SQ SEQUENCE 343 AA; 38050 MW; 462EB159438C5BEF CRC64;

Query Match 73.3%; Score 33; DB 1; Length 343;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8
DB 62 VLGLRDYK 69

Search completed: October 11, 2002, 14:46:14
Job time : 12 secs
```



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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:44:09 ; Search time 21 seconds  
(without alignments)  
36.605 Million cell updates/sec

Title: US-09-787-334-1

Perfect score: 45

Sequence: 1 ILGHRDYK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_71:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	359	2 A49973	prostanoid FP rece
2	45	100.0	362	2 A53058	prostaglandin F2-a
3	41	91.1	366	2 A49877	prostaglandin F re
4	41	91.1	366	2 S51281	F2-alpha receptor
5	41	91.1	366	2 I53488	prostaglandin F2 a
6	38	84.4	102	2 T44994	probable tryptopha
7	38	84.4	432	2 F64484	probable transamin
8	38	84.4	513	2 F84371	tryptophanyl-trna
9	37	82.2	304	2 C82045	5,10-methylenetet
10	37	82.2	364	2 E69131	tryptophan--trna 1
11	37	82.2	370	2 F64476	tryptophan--trna 1
12	36	80.0	157	2 JN0796	hypothetical 18.9K
13	36	80.0	420	2 E69461	tryptophanyl-trna
14	35	77.8	316	2 A83552	transcription regu
15	35	77.8	406	2 T39084	probable mannosylt
16	35	77.8	530	2 A84922	hypothetical prote
17	34	75.6	121	2 I48365	glucose transporta
18	34	75.6	151	2 D83552	hypothetical prote
19	34	75.6	380	2 D72641	probable chorismat
20	34	75.6	487	2 F82065	RNA polymerase sig
21	33	73.3	87	2 D81443	hypothetical prote
22	33	73.3	172	2 AF1663	hypothetical prote
23	33	73.3	172	2 AH1291	hypothetical prote
24	33	73.3	240	2 AB1305	phosphoribosylglyc
25	33	73.3	259	2 E64514	hypothetical prote
26	33	73.3	267	2 G90579	hypothetical prote
27	33	73.3	314	2 T02361	annexin P33 - maiz
28	33	73.3	343	2 F72319	translation initia
29	33	73.3	422	2 F89805	xanthine permease

30 33 73.3 428 2 A89950 glutamate-1-semial  
31 33 73.3 544 2 F82557 hypothetical prote  
32 33 73.3 1131 2 T41943 major DNA binding  
33 32 71.1 48 2 AE1891 hypothetical prote  
34 32 71.1 84 2 B89803 truncated integras  
35 32 71.1 98 2 A83976 hypothetical prote  
36 32 71.1 125 2 S21329 14K inner membrane  
37 32 71.1 180 2 D82550 conserved hypotet  
38 32 71.1 217 2 S74394 phosphoribosylglyc  
39 32 71.1 222 2 G72332 hypothetical prote  
40 32 71.1 245 1 TVMST2 transforming prote  
41 32 71.1 257 2 B83857 indol-3-glycerol p  
42 32 71.1 289 2 A98217 hemK protein homol  
43 32 71.1 289 2 A13069 protoporphylinogen  
44 32 71.1 291 2 A99181 xerC/D integrase-r  
45 32 71.1 350 2 AI0924 probable bacteriop

#### ALIGNMENTS

##### RESULT 1

A49973

prostanoid FP receptor - human

C:Species: Homo sapiens (man)

C:Date: 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 23-Jul-1999

C:Accession: A49973

R:Abramovitz, M.; Boie, Y.; Nguyen, T.; Rushmore, T.H.; Bayne, M.A.; Metters, K.M.; S

J. Biol. Chem. 269, 2632-2636, 1994

A:Title: Cloning and expression of a cDNA for the human prostanoid FP receptor.

A:Reference number: A49973; MUID:94132028

A:Accession: A49973

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-359 <ABR>

A:Cross-references: GB:L24470; NID:g456563; PIDN:AAAL7684.1; PID:g456564

C:Genetics:

A:Gene: GDB:PTGFR; FP

A:Cross-references: GDB:305480; OMIM:600563

A:Map position: lp31.1-lp31.1

C:Superfamily: prostaglandin E receptor EP1

C:Keywords: transmembrane protein

Query Match 100.0%; Score 45; DB 2; Length 359;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
|||||||  
Db 171 ILGHRDYK 178

##### RESULT 2

A53058

prostaglandin F2-alpha receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 02-Jun-1995 #sequence\_revision 02-Jun-1995 #text\_change 20-Jun-2000

C:Accession: A53058

R:Sakamoto, K.; Ezashi, T.; Miwa, K.; Okuda-Ashtaka, E.; Houtani, T.; Sugimoto, T.;

J. Biol. Chem. 269, 3881-3886, 1994

A:Title: Molecular cloning and expression of a cDNA of the bovine prostaglandin F-2a1

A:Reference number: A53058; MUID:94148901

A:Accession: A53058

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-362 <SAK>

A:Cross-references: GB:D17395; NID:g468435; PIDN:BAA04218.1; PID:g468436

C:Superfamily: prostaglandin E receptor EP1

Query Match 100.0%; Score 45; DB 2; Length 362;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
| | | | | | | |  
Db 171 ILGHRDYK 178

## RESULT 3

A49877  
prostaglandin F receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1995 #sequence\_revision 30-Jun-1995 #text\_change 20-Jun-2000  
C:Accession: A49877  
R:Sugimoto, Y.; Hasumoto, K.; Namba, T.; Irie, A.; Katsuyama, M.; Negishi, M.; Kakizuka, J. Biol. Chem. 269, 1356-1360, 1994  
A:Title: Cloning and expression of a cDNA for mouse prostaglandin F receptor.  
A:Reference number: A49877; MUID:94117451  
A:Accession: A49877  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-366 <SUG>  
A:Cross-references: GB:D17433; NID:g457656; PIDN:BAA04251.1; PID:g457657  
C:Superfamily: prostaglandin E receptor EP1  
C:Keywords: transmembrane protein

Query Match 91.1%; Score 41; DB 2; Length 366;  
Best Local Similarity 87.5%; Pred. No. 1.6;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
| | | | | | | |  
Db 171 ILGHRDYK 178

## RESULT 4

S51281  
P2-alpha receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 23-Jul-1999  
C:Accession: S51281  
R:de Vries, C.; Neuschaefer-Rube, F.; Haenecke, K.; Jungermann, K.; Pueschel, G.P.  
submitted to the EMBL Data Library, January 1995  
A:Reference number: S51281  
A:Accession: S51281  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-366 <DEV>  
A:Cross-references: EMBL:X83856; NID:g633625; PIDN:CAA58736.1; PID:g633626  
C:Superfamily: prostaglandin E receptor EP1

Query Match 91.1%; Score 41; DB 2; Length 366;  
Best Local Similarity 87.5%; Pred. No. 1.6;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
| | | | | | | |  
Db 171 ILGHRDYK 178

## RESULT 5

I53488  
prostaglandin F2 alpha receptor - rat  
C:Species: Rattus sp. (rat)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 23-Jul-1999  
C:Accession: I53488  
R:Lake, S.; Gullberg, H.; Wahlqvist, J.; Sjogren, A.M.; Kinult, A.; Lind, P.; Hellstrom  
FEBS Lett. 355, 317-325, 1994  
A:Title: Cloning of the rat and human prostaglandin F2 alpha receptors and the expressio  
A:Reference number: I53488; MUID:95080404  
A:Accession: I53488  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-366 <RES>  
A:Cross-references: GB:S74898; NID:g786610; PIDN:AAB32739.1; PID:g786611  
C:Superfamily: prostaglandin E receptor EP1

Query Match 91.1%; Score 41; DB 2; Length 366;  
Best Local Similarity 87.5%; Pred. No. 1.6;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
| | | | | | | |  
Db 171 ILGHRDYK 178

## RESULT 6

T44994  
probable tryptophanyl aminoacyl tRNA synthetase [imported] - Haloferax volcanii (frag  
C:Species: Haloferax volcanii  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 02-Sep-2000  
C:Accession: T44994  
R:Kleman-Leyer, K.; Armbruster, D.W.; Daniels, C.J.  
Cell 89, 839-847, 1997  
A:Title: Characterization of the Haloferax volcanii tRNA intron endonuclease gene rev  
A:Reference number: 222891; MUID:97344075  
A:Accession: T44994  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-102 <KLE>  
A:Cross-references: EMBL:AF001578; NID:g2160791; PIDN:AAC45447.1; PID:g2160793  
C:Genetics:  
C:Gene: trps  
C:Superfamily: mammalian tryptophan--tRNA ligase; amino acid--tRNA ligase repeat homo

Query Match 84.4%; Score 38; DB 2; Length 102;  
Best Local Similarity 75.0%; Pred. No. 1.7;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
| | | | | | | |  
Db 67 IFGHRDYR 74

## RESULT 7

F64484  
probable transaminase (EC 2.6.1.-) MJ1479 [similarity] - Methanococcus jannaschii  
N:Alternate names: alanine aminotransferase 2  
C:Species: Methanococcus jannaschii  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jun-2000  
C:Accession: F64484  
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak  
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,  
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese  
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc  
A:Reference number: A64300; MUID:96337999  
A:Accession: F64484  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-432 <BUL>  
A:Cross-references: GB:U67588; GB:L77117; NID:g1592111; PID:g1592118; TIGR:WJ1479; PI  
C:Genetics:  
C:Superfamily: aspartate transaminase  
C:Keywords: aminotransferase

Query Match 84.4%; Score 38; DB 2; Length 432;  
Best Local Similarity 75.0%; Pred. No. 7.9;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
| | | | | | | |  
Db 294 IMGHRNYK 301

## RESULT 8

F84371

tryptophanyl-tRNA synthetase [imported] - Halobacterium sp. NRC-1  
 C:Species: Halobacterium sp. NRC-1  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

A:Accession: F84371  
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1.  
 A:Reference number: A84160; MUID:20504483

A:Accession: F84371  
 A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-513 <STO>

A:Cross-references: GB:AE004437; NID:g10581625; PIDN:AAG20338.1; GSPDB:GN00138

C:Genetics:  
 A:Gene: trpSI

Query Match 84.4%; Score 38; DB 2; Length 513;

Best Local Similarity 75.0%; Pred. No. 9.5;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8

I I I I I I

Db 59 IFGHRDYR 66

RESULT 9

C82045

5,10-methylenetetrahydrofolate reductase VC2685 [imported] - Vibrio cholerae (strain N16  
 C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001

C:Accession: C82045

R:Heidelber, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

ardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833

A:Accession: C82045

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-304 <HEI>

A:Cross-references: GB:AE004335; GB:AE003852; NID:g9657289; PIDN:AAF95826.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC2685

A:Map position: 1

C:Superfamily: 5,10-methylenetetrahydrofolate reductase (FADH2)

Query Match 82.2%; Score 37; DB 2; Length 304;

Best Local Similarity 85.7%; Pred. No. 8.7;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGHRDYK 8

I I I I I I

Db 3 LGHREYK 9

RESULT 10

E69131

tryptophan--tRNA ligase (EC 6.1.1.2) - Methanobacterium thermoautotrophicum (strain Del

N:Alternate names: tryptophanyl-tRNA synthetase

C:Species: Methanobacterium thermoautotrophicum

C:Date: 03-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999

C:Accession: E69131

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Ol, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.

kl, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7133-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A:Reference number: A69000; MUID:98037514

A:Accession: E69131

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-364 <MTH>

A:Cross-references: GB:AE000812; GB:AE000666; NID:g2621298; PIDN:AAB84757.1; PID:g262

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH251

A:Start codon: TTG

C:Superfamily: mammalian tryptophan--tRNA ligase; amino acid--tRNA ligase repeat homo

C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 82.2%; Score 37; DB 2; Length 364;

Best Local Similarity 75.0%; Pred. No. 11;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8

I I I I I I

Db 43 IFGHRDYE 50

RESULT 11

F64476

tryptophan--tRNA ligase (EC 6.1.1.2) - Methanococcus jannaschii

N:Alternate names: tryptophanyl-tRNA synthetase

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000

C:Accession: F64476

R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak

; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc

A:Reference number: A64300; MUID:96337999

A:Accession: F64476

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-370 <BUL>

A:Cross-references: GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB599425.1; PID:g1592065

C:Genetics:

A:Map position: FOR1375885-1376997

A:Start codon: GTG

C:Superfamily: mammalian tryptophan--tRNA ligase; amino acid--tRNA ligase repeat homo

C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 82.2%; Score 37; DB 2; Length 370;

Best Local Similarity 75.0%; Pred. No. 11;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8

I I I I I I

Db 48 ILGHRDFE 55

RESULT 12

JN0796

hypothetical 18.9K protein - Clostridium acetobutylicum (strain NCIMB 8052)

N:Alternate names: ORF4 protein

C:Species: Clostridium acetobutylicum

C:Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 15-Oct-1999

C:Accession: JN0796

R:Oultram, J.D.; Burr, I.D.; Elmore, M.J.; Minton, N.P.

Gene 131, 107-112, 1993

A:Title: Cloning and sequence analysis of the genes encoding phosphotransbutyrylase a

A:Reference number: PN0619; MUID:93380658

A:Accession: JN0796

A:Molecule type: DNA

A:Residues: 1-157 <OUL>

A:Cross-references: GB:L04468; NID:g144890; PIDN:AAAS2082.1; PID:g144894

Query Match 80.0%; Score 36; DB 2; Length 157;

Best Local Similarity 87.5%; Pred. No. 6.8;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8

|||||

Db 110 ILGHRDKK 117

#### RESULT 13

E69461

tryptophanyl-tRNA synthetase (trps) homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 21-Jul-2000

C:Accession: E69461

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A:Reference number: A69250; MUID:98049343

A:Accession: E69461

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-420 <KLE>

A:Cross-references: GB:AF000986; GB:AF000782; NID:g2689309; PIDN:AAB89554.1; PID:g264885

C:Superfamily: mammalian tryptophan--trna ligase; amino acid--trna ligase repeat homolog

Query Match 80.0%; Score 36; DB 2; Length 420;

Best Local Similarity 85.7%; Pred. No. 20;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILGHRDY 7

|||||

Db 45 IFGHRDY 51

#### RESULT 14

AH3552

transcription regulatory protein, lysR family BMEII0345 [imported] - Brucella melitensis

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002

C:Accession: AH3552

R:DelVecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:11756688

A:Accession: AH3552

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-316 <KUR>

A:Cross-references: GB:AF008918; PIDN:AAL53587.1; PID:g17984499; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEII0345

A:Map position: II

Query Match 77.8%; Score 35; DB 2; Length 316;

Best Local Similarity 85.7%; Pred. No. 23;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILGHRDY 7

|||||

Db 179 IYGHRDY 185

#### RESULT 15

T39084

probable mannosyltransferase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C:Accession: T39084

R:Gentles, S.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, September 1997

A:Reference number: Z21826

A:Accession: T39084

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-406 <GEN>

A:Cross-references: EMBL:Z99532; PIDN:CAB16723.2; GSPDB:GN00066; SPDB:SPAC7D4.06c

A:Experimental source: strain 972h-; cosmid c7D4

C:Genetics:

A:Gene: SPDB:SPAC7D4.06c

A:Map position: 1

Query Match 77.8%; Score 35; DB 2; Length 406;

Best Local Similarity 75.0%; Pred. No. 30;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8

|||||

Db 63 LLGERDYK 70

Search completed: October 11, 2002, 14:47:29

Job time : 24 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:45:14 ; Search time 16 Seconds  
(without alignments)  
12.213 Million cell updates/sec

Title: US-09-787-334-1  
Perfect score: 45  
Sequence: 1 ILGHRDYK 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2.6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2.6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2.6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2.6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2.6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	359	2	US-08-976-074-5
2	45	100.0	359	2	US-08-083-741-5
3	45	100.0	359	4	US-08-976-166A-5
4	41	91.1	366	1	US-08-554-612C-50
5	41	91.1	369	1	US-08-416-756A-2
6	41	91.1	390	1	US-08-416-756A-5
7	33	73.3	241	6	5175383-7
8	32	71.1	137	6	5175383-4
9	32	71.1	245	1	US-08-439-725A-11
10	32	71.1	245	2	US-08-867-471-11
11	32	71.1	245	2	US-08-438-439C-7
12	32	71.1	245	2	US-08-438-439C-17
13	32	71.1	245	3	US-08-705-245-12
14	32	71.1	439	1	US-08-190-802A-65
15	32	71.1	439	4	US-08-477-346-65
16	32	71.1	439	4	US-08-473-089-65
17	32	71.1	587	4	US-09-020-465-2
18	32	71.1	634	2	US-09-020-466-2
19	32	71.1	634	3	US-09-192-659-2
20	30	66.7	38	1	US-07-977-630-63
21	30	66.7	59	1	US-08-269-441A-12
22	30	66.7	95	1	US-08-341-219-2
23	30	66.7	95	4	US-08-912-314A-2
24	30	66.7	314	1	US-08-269-441A-2
25	30	66.7	314	4	US-09-008-465-3
26	30	66.7	314	4	US-09-276-851-2
27	30	66.7	341	4	US-09-008-465-1

Sequence 2, Appli  
Sequence 30, Appli  
Sequence 2, Appli  
Sequence 30, Appli  
Sequence 13, Appli  
Sequence 2, Appli  
Sequence 13, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 8, Appli  
Sequence 23, Appli  
Sequence 19, Appli  
Sequence 11, Appli  
Sequence 65, Appli  
Sequence 11, Appli  
Sequence 12, Appli

#### ALIGNMENTS

RESULT 1  
US-08-976-074-5  
; Sequence 5, Application US/08976074  
; Patent No. 5840847  
; GENERAL INFORMATION:  
; APPLICANT: ABRAMOVITZ, MARK  
; APPLICANT: GRYGORCZYK, RICHARD  
; APPLICANT: METTERS, KATHLEEN  
; APPLICANT: NGUYEN, TRUYEN  
; APPLICANT: RUSHMORE, THOMAS H.  
; APPLICANT: SLIPETZ, DEBORAH  
; TITLE OF INVENTION: DNA Encoding Prostaglandin Receptor FP  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: J. Mark Hand - Merck & Co., Inc.  
; STREET: P.O. Box 2000 - 126 E. Lincoln Avenue  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07065  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/976,074  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HAND, J. MARK  
; REGISTRATION NUMBER: 36,545  
; REFERENCE/DOCKET NUMBER: 19027DA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (732) 594-3905  
; TELEFAX: (732) 594-4720  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 359 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-976-074-5

Query Match 100.0%; Score 45; DB 2; Length 359;  
Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;  
QY 1 ILGHRDYK 8



TELEFAX: (415) 854-0875  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 366 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-554-612C-50

Query Match 91.1%; Score 41; DB 1; Length 366;  
Best Local Similarity 87.5%; Pred. No. 1.1;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
|||||  
Db 171 ILGHRDYQ 178

RESULT 5  
US-08-416-756A-2  
; Sequence 2, Application US/08416756A  
; Patent No. 5750369  
; GENERAL INFORMATION:  
; APPLICANT: Lake, Staffan  
; APPLICANT: Stjernschantz, Johan  
; TITLE OF INVENTION: DNA Encoding A Prostaglandin F2' Receptor, A  
; TITLE OF INVENTION: Host Cell Transformed Therewith and An Expression Product  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N. W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/416,756A  
; FILING DATE: 13-APR-1990  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: WO PCT/SE93/00789  
; FILING DATE: 01-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cimbala, Michele A.  
; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 1370.0070000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 369 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-416-756A-5

Query Match 91.1%; Score 41; DB 1; Length 369;  
Best Local Similarity 87.5%; Pred. No. 1.1;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
|||||  
Db 174 ILGHRDYQ 181

RESULT 6  
US-08-416-756A-5  
; Sequence 5, Application US/08416756A  
; Patent No. 5750369  
; GENERAL INFORMATION:  
; APPLICANT: Lake, Staffan  
; APPLICANT: Stjernschantz, Johan  
; TITLE OF INVENTION: DNA Encoding A Prostaglandin F2' Receptor, A  
; TITLE OF INVENTION: Host Cell Transformed Therewith and An Expression Product  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N. W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/416,756A  
; FILING DATE: 13-APR-1990  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: WO PCT/SE93/00789  
; FILING DATE: 01-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cimbala, Michele A.  
; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 1370.0070000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 390 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-416-756A-5

Query Match 91.1%; Score 41; DB 1; Length 390;  
Best Local Similarity 87.5%; Pred. No. 1.2;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ILGHRDYK 8  
|||||  
Db 174 ILGHRDYQ 181

RESULT 7  
5175383-7  
; Patent No. 5175383  
; APPLICANT: LEDER, PHILIP; MULLER, WILLIAM J.  
; TITLE OF INVENTION: ANIMAL MODEL FOR BENIGN PROSTATIC DISEASE  
; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION NUMBER: US/07/312,641  
; FILING DATE: 17-FEB-1989  
; SEQ ID NO: 7:  
; LENGTH: 241  
5175383-7

Query Match 73.3%; Score 33; DB 6; Length 241;  
Best Local Similarity 50.0%; Pred. No. 28;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8  
:||||:|:  
Db 181 VLGHKDH 188

RESULT 8  
5175383-4  
; Patent No. 5175383  
; APPLICANT: LEDER, PHILIP; MULLER, WILLIAM J.  
; TITLE OF INVENTION: ANIMAL MODEL FOR BENIGN PROSTATIC DISEASE  
; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/312,641  
; FILING DATE: 17-FEB-1989  
; SEQ ID NO: 4  
; LENGTH: 137  
5175383-4

Query Match 71.1%; Score 32; DB 6; Length 137;  
Best Local Similarity 50.0%; Pred. No. 25;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8  
:||||:|:  
-Db 74 VLGHKDH 81

RESULT 9  
US-08-439-725A-11  
; Sequence 11, Application US/08439725A  
; Patent No. 5693775  
; GENERAL INFORMATION:  
; APPLICANT: Nathans, Jeremy  
; APPLICANT: Smallwood, Philip M.  
; APPLICANT: Macke, Jennifer P.  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS  
; TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/439,725A  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halle, Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07265/047001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 617/678-5099  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 245 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-439-725A-11

Query Match 71.1%; Score 32; DB 1; Length 245;  
Best Local Similarity 50.0%; Pred. No. 46;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8  
:||||:|:  
Db 182 VLGHKDH 189

RESULT 10  
US-08-867-471-11  
; Sequence 11, Application US/08867471  
; Patent No. 5872226  
; GENERAL INFORMATION:  
; APPLICANT: Nathans, Jeremy  
; APPLICANT: Smallwood, Philip M.  
; APPLICANT: Macke, Jennifer P.  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS  
; TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/867,471  
; FILING DATE: 02-JUN-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/439,725  
; FILING DATE: 12-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halle, Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07265/047001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 617/678-5099  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 245 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-867-471-11

Query Match 71.1%; Score 32; DB 2; Length 245;  
Best Local Similarity 50.0%; Pred. No. 46;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8  
:||||:|:  
Db 182 VLGHKDH 189

RESULT 11  
US-08-438-439C-7  
; Sequence 7, Application US/08438439C  
; Patent No. 5876967  
; GENERAL INFORMATION:  
; APPLICANT: Nathans, Jeremy  
; APPLICANT: Smallwood, Philip M.  
; APPLICANT: Macke, Jennifer P.



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; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,439C
; FILING DATE: May 12, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/046001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-438-439C-7

Query Match 71.1%; Score 32; DB 2; Length 245;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8
Db 182 VLGHKDHE 189

; RESULT 12
; US-08-438-439C-17
; Sequence 17, Application US/08438439C
; Patent No. 5876967
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Phillip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,439C
; FILING DATE: May 12, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Lisa A.
```

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; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/046001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-438-439C-17

Query Match 71.1%; Score 32; DB 2; Length 245;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8
Db 182 VLGHKDHE 189

; RESULT 13
; US-08-705-245-12
; Sequence 12, Application US/08705245
; Patent No. 6020189
; GENERAL INFORMATION:
; APPLICANT: Nathans et al., Jeremy
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTORS (FHFs) AND METHODS OF USE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,245
; FILING DATE: 30-AUG-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/094001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-50999
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-705-245-12

Query Match 71.1%; Score 32; DB 3; Length 245;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILGHRDYK 8
Db 182 VLGHKDHE 189
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## RESULT 14

US-08-190-802A-65  
; Sequence 65, Application US/08190802A  
; Patent No. 5519003  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Ron, Dorit  
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Denlinger & Associates  
; STREET: P.O. Box 60850  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306-0850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/190.802A  
; FILING DATE: 01-FEB-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fabian, Gary R.  
; REGISTRATION NUMBER: 33,875  
; REFERENCE/DOCKET NUMBER: 8600-0139  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 439 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: YC07, Fig. 48  
US-08-190-802A-65

Query Match 71.1%; Score 32; DB 1; Length 439;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GHRDY 7  
Db 17 GHRDY 21

## RESULT 15

US-08-477-346-65  
; Sequence 65, Application US/08477346  
; Patent No. 6262023  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; APPLICANT: Ron, Dorit  
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 2000 Pennsylvania Avenue, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477.346  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/487,072  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 2550-0025.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 439 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: YC07, Fig. 48  
US-08-477-346-65

Query Match 71.1%; Score 32; DB 4; Length 439;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GHRDY 7  
Db 17 GHRDY 21

Search completed: October 11, 2002, 14:47:55  
Job time : 17 secs